

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

- (i) APPLICANT: Ni et al.
- (ii) TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR INHIBITOR
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
  - (B) STREET: 1100 NEW YORK AVENUE, SUITE 600
  - (C) CITY: WASHINGTON
  - (D) STATE: DC
  - (E) COUNTRY: USA
  - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US To be assigned
  - (B) FILING DATE: Herewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/934,011
  - (B) FILING DATE: 15-AUG-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/024,056
  - (B) FILING DATE: 16-AUG-1996
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: STEFFE, ERIC K.
  - (B) REGISTRATION NUMBER: 36,688
  - (C) REFERENCE/DOCKET NUMBER: 1488.0300002
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 202-371-2600
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### (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1371 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS

(B) LOCATION: 67..1242

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 109..1242

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 67..108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGGG AAAACTCTAT TTTGAAAATG AATATATTTT GATTTAAACA ATACAGAGAA	60
GTCAAA ATG GAC ACA ATC TTC TTG TGG AGT CTT CTA TTG CTG TTT TTT	108
Met Asp Thr Ile Phe Leu Trp Ser Leu Leu Leu Phe Phe	
-14 -10 -5	
GGA AGT CAA GCC TCA AGA TGC TCA GCT CAA AAA AAT ACC GAA TTT GCA	156
Gly Ser Gln Ala Ser Arg Cys Ser Ala Gln Lys Asn Thr Glu Phe Ala	
1 5 10 15	
GTG GAT CTT TAT CAA GAG GTT TCC TTA TCT CAT AAG GAC AAC ATT ATA	204
Val Asp Leu Tyr Gln Glu Val Ser Leu Ser His Lys Asp Asn Ile Ile	
20 25 30	
TTT TCA CCC CTT GGA ATA ACT TTG GTT CTT GAG ATG GTA CAA CTG GGA	252
Phe Ser Pro Leu Gly Ile Thr Leu Val Leu Glu Met Val Gln Leu Gly	
35 40 45	
GCC AAA GGA AAA GCA CAG CAG CAG ATA AGA CAA ACT TTA AAA CAA CAG	300
Ala Lys Gly Lys Ala Gln Gln Gln Ile Arg Gln Thr Leu Lys Gln Gln	
50 55 60	
GAA ACC TCA GCT GGG GAA GAA TTT TTG GTA CTG AAG TCA TTT TGC TCT	348
Glu Thr Ser Ala Gly Glu Glu Phe Leu Val Leu Lys Ser Phe Cys Ser	
65 70 75 80	
GCC ATC TCA GAG AAA AAA CAA GAA TTT ACA TTT AAT CTT GCC AAT GCC	396
Ala Ile Ser Glu Lys Lys Gln Glu Phe Thr Phe Asn Leu Ala Asn Ala	
85 90 95	
CTC TAC CTT CAA GAA GGA TTC ACT GTG AAA GAA CAG TAT CTC CAT GGC	444
Leu Tyr Leu Gln Glu Gly Phe Thr Val Lys Glu Gln Tyr Leu His Gly	
100 105 110	
AAC AAG GAA TTT TTT CAG AGT GCT ATA AAA CTG GTG GAT TTT CAA GAT	492
Asn Lys Glu Phe Phe Gln Ser Ala Ile Lys Leu Val Asp Phe Gln Asp	
115 120 125	
GCA AAG GCT TGT GCA GAG ATG ATA AGT ACC TGG GTA GAA AGA AAA ACA	540
Ala Lys Ala Cys Ala Glu Met Ile Ser Thr Trp Val Glu Arg Lys Thr	
130 135 140	
GAT GGA AAA ATT AAA GAC ATG TTT TCA GGG GAA GAA TTT GGC CCT CTG	588
Asp Gly Lys Ile Lys Asp Met Phe Ser Gly Glu Glu Phe Gly Pro Leu	
145 150 155 160	
ACT CGG CTT GTC CTG GTG AAT GCT ATT TAT TTC AAA GGA GAT TGG AAA	636
Thr Arg Leu Val Leu Val Asn Ala Ile Tyr Phe Lys Gly Asp Trp Lys	
165 170 175	

CAG AAA TTC AGA AAA GAG GAC ACA CAG CTG ATA AAT TTT ACT AAG AAA Gln Lys Phe Arg Lys Glu Asp Thr Gln Leu Ile Asn Phe Thr Lys Lys 180 185 190	684
AAT GGT TCA ACT GTC AAA ATT CCA ATG ATG AAG GCT CTT CTG AGA ACA Asn Gly Ser Thr Val Lys Ile Pro Met Met Lys Ala Leu Leu Arg Thr 195 200 205	732
AAA TAT GGT TAT TTT TCT GAA TCT TCC CTG AAC TAC CAA GTT TTA GAA Lys Tyr Gly Tyr Phe Ser Glu Ser Ser Leu Asn Tyr Gln Val Leu Glu 210 215 220	780
TTG TCT TAC AAA GGT GAT GAA TTT AGC TTA ATT ATC ATA CTT CCT GCA Leu Ser Tyr Lys Gly Asp Glu Phe Ser Leu Ile Ile Ile Leu Pro Ala 225 230 235 240	828
GAA GGT ATG GAT ATA GAA GAA GTG GAA AAA CTA ATT ACT GCT CAA CAA Glu Gly Met Asp Ile Glu Glu Val Glu Lys Leu Ile Thr Ala Gln Gln 245 250 255	876
ATC CTA AAA TGG CTC TCT GAG ATG CAA GAA GAG GAA GTA GAA ATA AGC Ile Leu Lys Trp Leu Ser Glu Met Gln Glu Glu Glu Val Glu Ile Ser 260 265 270	924
CTC CCT AGA TTT AAA GTA GAA CAA AAA GTA GAC TTC AAA GAC GTT TTG Leu Pro Arg Phe Lys Val Glu Gln Lys Val Asp Phe Lys Asp Val Leu 275 280 285	972
TAT TCT TTG AAC ATA ACC GAG ATA TTT AGT GGT GGC TGC GAC CTT TCT Tyr Ser Leu Asn Ile Thr Glu Ile Phe Ser Gly Gly Cys Asp Leu Ser 290 295 300	1020
GGA ATA ACA GAT TCA TCT GAA GTG TAT GTT TCC CAA GTG ACG CAA AAA Gly Ile Thr Asp Ser Ser Glu Val Tyr Val Ser Gln Val Thr Gln Lys 305 310 315 320	1068
GTT TTC TTT GAG ATA AAT GAA GAT GGT AGT GAA GCT GCA ACA TCA ACT Val Phe Phe Glu Ile Asn Glu Asp Gly Ser Glu Ala Ala Thr Ser Thr 325 330 335	1116
GGC ATA CAC ATC CCT GTG ATC ATG AGT CTG GCT CAA AGC CAA TTT ATA Gly Ile His Ile Pro Val Ile Met Ser Leu Ala Gln Ser Gln Phe Ile 340 345 350	1164
GCA AAT CAT CCA TTT CTG TTT ATT ATG AAG CAT AAT CCA ACA GAA TCA Ala Asn His Pro Phe Leu Phe Ile Met Lys His Asn Pro Thr Glu Ser 355 360 365	1212
ATT CTG TTT ATG GGA AGA GTG ACA AAT CCC TGACACCCAG GAGATAAAAG Ile Leu Phe Met Gly Arg Val Thr Asn Pro 370 375	1262
GAAGAGATTT AGATTCACTG TGAATGAAAA GCACAGCCTC AGAATAAAAG ATGATTTCTC	1322
AAAAATAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1371

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 392 amino acids
  - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Thr	Ile	Phe	Leu	Trp	Ser	Leu	Leu	Leu	Leu	Phe	Phe	Gly	Ser	
-14				-10					-5					1		
Gln	Ala	Ser	Arg	Cys	Ser	Ala	Gln	Lys	Asn	Thr	Glu	Phe	Ala	Val	Asp	
		5					10					15				
Leu	Tyr	Gln	Glu	Val	Ser	Leu	Ser	His	Lys	Asp	Asn	Ile	Ile	Phe	Ser	
	20					25					30					
Pro	Leu	Gly	Ile	Thr	Leu	Val	Leu	Glu	Met	Val	Gln	Leu	Gly	Ala	Lys	
	35				40					45					50	
Gly	Lys	Ala	Gln	Gln	Gln	Ile	Arg	Gln	Thr	Leu	Lys	Gln	Gln	Glu	Thr	
			55						60					65		
Ser	Ala	Gly	Glu	Glu	Phe	Leu	Val	Leu	Lys	Ser	Phe	Cys	Ser	Ala	Ile	
			70					75					80			
Ser	Glu	Lys	Lys	Gln	Glu	Phe	Thr	Phe	Asn	Leu	Ala	Asn	Ala	Leu	Tyr	
		85					90					95				
Leu	Gln	Glu	Gly	Phe	Thr	Val	Lys	Glu	Gln	Tyr	Leu	His	Gly	Asn	Lys	
	100					105					110					
Glu	Phe	Phe	Gln	Ser	Ala	Ile	Lys	Leu	Val	Asp	Phe	Gln	Asp	Ala	Lys	
	115				120					125					130	
Ala	Cys	Ala	Glu	Met	Ile	Ser	Thr	Trp	Val	Glu	Arg	Lys	Thr	Asp	Gly	
			135						140					145		
Lys	Ile	Lys	Asp	Met	Phe	Ser	Gly	Glu	Glu	Phe	Gly	Pro	Leu	Thr	Arg	
			150					155					160			
Leu	Val	Leu	Val	Asn	Ala	Ile	Tyr	Phe	Lys	Gly	Asp	Trp	Lys	Gln	Lys	
	165						170					175				
Phe	Arg	Lys	Glu	Asp	Thr	Gln	Leu	Ile	Asn	Phe	Thr	Lys	Lys	Asn	Gly	
	180					185					190					
Ser	Thr	Val	Lys	Ile	Pro	Met	Met	Lys	Ala	Leu	Leu	Arg	Thr	Lys	Tyr	
	195				200					205					210	
Gly	Tyr	Phe	Ser	Glu	Ser	Ser	Leu	Asn	Tyr	Gln	Val	Leu	Glu	Leu	Ser	
			215						220					225		
Tyr	Lys	Gly	Asp	Glu	Phe	Ser	Leu	Ile	Ile	Ile	Leu	Pro	Ala	Glu	Gly	
		230						235					240			
Met	Asp	Ile	Glu	Glu	Val	Glu	Lys	Leu	Ile	Thr	Ala	Gln	Gln	Ile	Leu	
	245						250					255				
Lys	Trp	Leu	Ser	Glu	Met	Gln	Glu	Glu	Glu	Val	Glu	Ile	Ser	Leu	Pro	
	260					265					270					
Arg	Phe	Lys	Val	Glu	Gln	Lys	Val	Asp	Phe	Lys	Asp	Val	Leu	Tyr	Ser	
	275				280					285					290	



145		150		155		160									
Asp	Trp	Val	Lys	Thr	His	Thr	Lys	Gly	Met	Ile	Ser	Asn	Leu	Leu	Gly
				165					170					175	
Lys	Gly	Ala	Val	Asp	Gln	Leu	Thr	Arg	Leu	Val	Leu	Val	Asn	Ala	Leu
			180					185					190		
Tyr	Phe	Asn	Gly	Gln	Trp	Lys	Thr	Pro	Phe	Pro	Asp	Ser	Ser	Thr	His
		195					200					205			
Arg	Arg	Leu	Phe	His	Lys	Ser	Asp	Gly	Ser	Thr	Val	Ser	Val	Pro	Met
	210					215					220				
Met	Ala	Gln	Thr	Asn	Lys	Phe	Asn	Tyr	Thr	Glu	Phe	Thr	Thr	Pro	Asp
225					230					235					240
Gly	His	Tyr	Tyr	Asp	Ile	Leu	Glu	Leu	Pro	Tyr	His	Gly	Asp	Thr	Leu
				245					250					255	
Ser	Met	Phe	Ile	Ala	Ala	Pro	Tyr	Glu	Lys	Glu	Val	Pro	Leu	Ser	Ala
			260					265					270		
Leu	Thr	Asn	Ile	Leu	Ser	Ala	Gln	Leu	Ile	Ser	His	Trp	Lys	Gly	Asn
		275					280					285			
Met	Thr	Arg	Leu	Pro	Arg	Leu	Leu	Val	Leu	Pro	Lys	Phe	Ser	Leu	Glu
	290					295					300				
Thr	Glu	Val	Asp	Leu	Arg	Lys	Pro	Leu	Glu	Asn	Leu	Gly	Met	Thr	Asp
305					310					315					320
Met	Phe	Arg	Gln	Phe	Gln	Ala	Asp	Phe	Thr	Ser	Leu	Ser	Asp	Gln	Glu
				325					330					335	
Pro	Leu	His	Val	Ala	Gln	Ala	Leu	Gln	Lys	Val	Lys	Ile	Glu	Val	Asn
			340					345					350		
Glu	Ser	Gly	Thr	Val	Ala	Ser	Ser	Ser	Thr	Ala	Val	Ile	Val	Ser	Ala
		355					360					365			
Arg	Met	Ala	Pro	Glu	Glu	Ile	Ile	Met	Asp	Arg	Pro	Phe	Leu	Phe	Val
	370					375					380				
Val	Arg	His	Asn	Pro	Thr	Gly	Thr	Val	Leu	Phe	Met	Gly	Gln	Val	Met
385					390					395					400
Glu	Pro														

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 415 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Glu	Asp	Leu	Cys	Val	Ala	Asn	Thr	Leu	Phe	Ala	Leu	Asn	Leu	Phe	1	5	10	15
Lys	His	Leu	Ala	Lys	Ala	Ser	Pro	Thr	Gln	Asn	Leu	Phe	Leu	Ser	Pro	20	25	30	
Trp	Ser	Ile	Ser	Ser	Thr	Met	Ala	Met	Val	Tyr	Met	Gly	Ser	Arg	Gly	35	40	45	
Ser	Thr	Glu	Asp	Gln	Met	Ala	Lys	Val	Leu	Gln	Phe	Asn	Glu	Val	Gly	50	55	60	
Ala	Asn	Ala	Val	Thr	Pro	Met	Thr	Pro	Glu	Asn	Phe	Thr	Ser	Cys	Gly	65	70	75	
Phe	Met	Gln	Gln	Ile	Gln	Lys	Gly	Ser	Tyr	Pro	Asp	Ala	Ile	Leu	Gln	85	90	95	
Ala	Gln	Ala	Ala	Asp	Lys	Ile	His	Ser	Ser	Phe	Arg	Ser	Leu	Ser	Ser	100	105	110	
Ala	Ile	Asn	Ala	Ser	Thr	Gly	Asp	Tyr	Leu	Leu	Glu	Ser	Val	Asn	Lys	115	120	125	
Leu	Phe	Gly	Glu	Lys	Ser	Ala	Ser	Phe	Arg	Glu	Glu	Tyr	Ile	Arg	Leu	130	135	140	
Cys	Gln	Lys	Tyr	Tyr	Ser	Ser	Glu	Pro	Gln	Ala	Val	Asp	Phe	Leu	Glu	145	150	155	
Cys	Ala	Glu	Glu	Ala	Arg	Lys	Lys	Ile	Asn	Ser	Trp	Val	Lys	Thr	Gln	165	170	175	
Thr	Lys	Gly	Lys	Ile	Pro	Asn	Leu	Leu	Pro	Glu	Gly	Ser	Val	Asp	Gly	180	185	190	
Asp	Thr	Arg	Met	Val	Leu	Val	Asn	Ala	Val	Tyr	Phe	Lys	Gly	Lys	Trp	195	200	205	
Lys	Thr	Pro	Phe	Glu	Lys	Lys	Leu	Asn	Gly	Leu	Tyr	Pro	Phe	Arg	Val	210	215	220	
Asn	Ser	Ala	Gln	Arg	Thr	Pro	Val	Gln	Met	Met	Tyr	Leu	Arg	Glu	Lys	225	230	235	
Leu	Asn	Ile	Gly	Tyr	Ile	Glu	Asp	Leu	Lys	Ala	Gln	Ile	Leu	Glu	Leu	245	250	255	
Pro	Tyr	Ala	Gly	Asp	Val	Ser	Met	Phe	Leu	Leu	Leu	Pro	Asp	Glu	Ile	260	265	270	
Ala	Asp	Val	Ser	Thr	Gly	Leu	Glu	Leu	Leu	Glu	Ser	Glu	Ile	Thr	Tyr	275	280	285	
Asp	Lys	Leu	Asn	Lys	Trp	Thr	Ser	Lys	Asp	Lys	Met	Ala	Glu	Asp	Glu	290	295	300	
Val	Glu	Val	Tyr	Ile	Pro	Gln	Phe	Lys	Leu	Glu	Glu	His	Tyr	Glu	Leu	305	310	315	

Arg	Ser	Ile	Leu	Arg	Ser	Met	Gly	Met	Glu	Asp	Ala	Phe	Asn	Lys	Gly
				325					330					335	
Arg	Ala	Asn	Phe	Ser	Gly	Met	Ser	Glu	Arg	Asn	Asp	Leu	Phe	Leu	Ser
			340					345					350		
Glu	Val	Phe	His	Gln	Ala	Met	Val	Asp	Val	Asn	Glu	Glu	Gly	Thr	Glu
		355					360					365			
Ala	Ala	Ala	Gly	Thr	Gly	Gly	Val	Met	Thr	Gly	Arg	Thr	Gly	His	Gly
		370				375					380				
Gly	Pro	Gln	Phe	Val	Ala	Asp	His	Pro	Phe	Leu	Phe	Leu	Ile	Met	His
385					390					395					400
Lys	Ile	Thr	Lys	Cys	Ile	Leu	Phe	Phe	Gly	Arg	Phe	Cys	Ser	Pro	
				405					410					415	

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGCCCATGGG AAGTCAAGCC TCAAG

25

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGCAAGCTTT CACTTCCTTT TATCTCCCTG

30

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGCGGATCCG CCATCATGGA CACAATCTTC TTG 33

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGGTACCT CACTTCCTTT TATCTCCCTG 30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCTCTAGAT CAAGCGTAGT CTGGGACGTC GTATGGGTAG GGATTTGTCA CTCTTCC 57

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

NAATATATTT NNATTTAAAC AATACAGAGA AGTCAAAATG GACACAATCT TCTTGTGGAG 60

TCTTCTATTG CTGTTTTTTC GAAGTCAAGC CTCANGAATG CTCAGCTGCA AAAAAATACC 120

GAATTTGCCA GTGGNATCTT TATCAAGAGG TTTCCCTTCAT CTGCATAAGG N 171

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 515 base pairs  
  (B) TYPE: nucleic acid  
  (C) STRANDEDNESS: single  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCANNANAA CAATCTNATC CAAGGACTGT GGNACTCCTG TTCCCTGCTC ATCATGTCAT	60
GGGGCATCTG CCAGGAACCA TCTTTGATGG TGTA AAAAATC TTGAATACAT AAGAGGGAAA	120
TTT TAGACTT GTTAGAAAGA AGCCAAGCAA TTGAGACCTT AGATAGAACT TAGAATTCTC	180
GCCGAGTTTT GTTGGGTAAT TGTTACTTCA AAAAAAATG CAATTTCTGT TCCCTCTTTC	240
CTCCAACCAT TTATCTGGGA AGCAAGTTAT TGGCAACCCA GAGCTGATTG TTGGAGCCGG	300
GGAAAATGGT GTGAAATGTG AGAAAATGTA ATTGAGATAA TAAAAACAAA AGATTTTACA	360
ATATATTATC CTCTAAGTCA TCCATTAAAA AATTGGTAGC AAAAATGTGC AGTGTTTCAA	420
GACTTTTCTT TTCTTTTTTT TTNAATACCA GATTAAAGTA GACCAAAAAG TAGACTCCAA	480
AGACGTTTGG ATNCTTGAAC ATAACCGNGA TATTA	515

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
  (A) LENGTH: 1370 base pairs  
  (B) TYPE: nucleic acid  
  (C) STRANDEDNESS: single  
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
  (B) LOCATION: 67..1281

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
  (B) LOCATION: 67..120

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
  (B) LOCATION: 121..1281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCACGAGGG AAAACTCTAT TTTGAAAATG AATATATTTT GATTTAAACA ATACAGAGAA	60
GTCAAA ATG GAC ACA ATC TTC TTG TGG AGT CTT CTA TTG CTG TTT TTT	108

	Met	Asp	Thr	Ile	Phe	Leu	Trp	Ser	Leu	Leu	Leu	Leu	Phe	Phe	
	-18			-15				-10						-5	
GGA	AGT	CAA	GCC	TCA	AGA	TGC	TCA	GCT	CAA	AAA	AAT	ACC	GAA	TTT	GCA
Gly	Ser	Gln	Ala	Ser	Arg	Cys	Ser	Ala	Gln	Lys	Asn	Thr	Glu	Phe	Ala
				1				5					10		
															156
GTG	GAT	CTT	TAT	CAA	GAG	GTT	TCC	TTA	TCT	CAT	AAG	GAC	AAC	ATT	ATA
Val	Asp	Leu	Tyr	Gln	Glu	Val	Ser	Leu	Ser	His	Lys	Asp	Asn	Ile	Ile
		15					20					25			
															204
TTT	TCA	CCC	CTT	GGA	ATA	ACT	TTG	GTT	CTT	GAG	ATG	GTA	CAA	CTG	GGA
Phe	Ser	Pro	Leu	Gly	Ile	Thr	Leu	Val	Leu	Glu	Met	Val	Gln	Leu	Gly
	30					35					40				
															252
GCC	AAA	GGA	AAA	GCA	CAG	CAG	CAG	ATA	AGA	CAA	ACT	TTA	AAA	CAA	CAG
Ala	Lys	Gly	Lys	Ala	Gln	Gln	Gln	Ile	Arg	Gln	Thr	Leu	Lys	Gln	Gln
	45				50					55					60
															300
GAA	ACC	TCA	GCT	GGG	GAA	GAA	TTT	TTG	GTA	CTG	AAG	TCA	TTT	TGC	TCT
Glu	Thr	Ser	Ala	Gly	Glu	Glu	Phe	Leu	Val	Leu	Lys	Ser	Phe	Cys	Ser
				65					70					75	
															348
GCC	ATC	TCA	GAG	AAA	AAA	CAA	GAA	TTT	ACA	TTT	AAT	CTT	GCC	AAT	GCC
Ala	Ile	Ser	Glu	Lys	Lys	Gln	Glu	Phe	Thr	Phe	Asn	Leu	Ala	Asn	Ala
			80					85					90		
															396
CTC	TAC	CTT	CAA	GAA	GGA	TTC	ACT	GTG	AAA	GAA	CAG	TAT	CTC	CAT	GGC
Leu	Tyr	Leu	Gln	Glu	Gly	Phe	Thr	Val	Lys	Glu	Gln	Tyr	Leu	His	Gly
		95					100					105			
															444
AAC	AAG	GAA	TTT	TTT	CAG	AGT	GCT	ATA	AAA	CTG	GTG	GAT	TTT	CAA	GAT
Asn	Lys	Glu	Phe	Phe	Gln	Ser	Ala	Ile	Lys	Leu	Val	Asp	Phe	Gln	Asp
	110					115					120				
															492
GCA	AAG	GCT	TGT	GCA	GAG	ATG	ATA	AGT	ACC	TGG	GTA	GAA	AGA	AAA	ACA
Ala	Lys	Ala	Cys	Ala	Glu	Met	Ile	Ser	Thr	Trp	Val	Glu	Arg	Lys	Thr
	125				130					135					140
															540
GAT	GGA	AAA	ATT	AAA	GAC	ATG	TTT	TCA	GGG	GAA	GAA	TTT	GGC	CCT	CTG
Asp	Gly	Lys	Ile	Lys	Asp	Met	Phe	Ser	Gly	Glu	Glu	Phe	Gly	Pro	Leu
				145					150					155	
															588
ACT	CGG	CTT	GTC	CTG	GTG	AAT	GCT	ATT	TAT	TTC	AAA	GGA	GAT	TGG	AAA
Thr	Arg	Leu	Val	Leu	Val	Asn	Ala	Ile	Tyr	Phe	Lys	Gly	Asp	Trp	Lys
			160				165						170		
															636
CAG	AAA	TTC	AGA	AAA	GAG	GAC	ACA	CAG	CTG	ATA	AAT	TTT	ACT	AAG	AAA
Gln	Lys	Phe	Arg	Lys	Glu	Asp	Thr	Gln	Leu	Ile	Asn	Phe	Thr	Lys	Lys
		175					180					185			
															684
AAT	GGT	TCA	ACT	GTC	AAA	ATT	CCA	ATG	ATG	AAG	GCT	CTT	CTG	AGA	ACA
Asn	Gly	Ser	Thr	Val	Lys	Ile	Pro	Met	Met	Lys	Ala	Leu	Leu	Arg	Thr
	190					195					200				
															732
AAA	TAT	GGT	TAT	TTT	TCT	GAA	TCT	TCC	CTG	AAC	TAC	CAA	GTT	TTA	GAA
Lys	Tyr	Gly	Tyr	Phe	Ser	Glu	Ser	Ser	Leu	Asn	Tyr	Gln	Val	Leu	Glu
	205				210					215					220
															780
TTG	TCT	TAC	AAA	GGT	GAT	GAA	TTT	AGC	TTA	ATT	ATC	ATA	CTT	CCT	GCA
Leu	Ser	Tyr	Lys	Gly	Asp	Glu	Phe	Ser	Leu	Ile	Ile	Ile	Leu	Pro	Ala
				225					230					235	
															828

GAA GGT ATG GAT ATA GAA GAA GTG GAA AAA CTA ATT ACT GCT CAA CAA	876
Glu Gly Met Asp Ile Glu Glu Val Glu Lys Leu Ile Thr Ala Gln Gln	
240 245 250	
ATC CTA AAA TGG CTC TCT GAG ATG CAA GAA GAG GAA GTA GAA ATA AGC	924
Ile Leu Lys Trp Leu Ser Glu Met Gln Glu Glu Glu Val Glu Ile Ser	
255 260 265	
CTC CCT AGA TTT AAA GTA GAA CAA AAA GTA GAC TTC AAA GAC GTT TTG	972
Leu Pro Arg Phe Lys Val Glu Gln Lys Val Asp Phe Lys Asp Val Leu	
270 275 280	
TAT TCT TTG AAC ATA ACC GAG ATA TTT AGT GGT GGC TGC GAC CTT TCT	1020
Tyr Ser Leu Asn Ile Thr Glu Ile Phe Ser Gly Gly Cys Asp Leu Ser	
285 290 295 300	
GGA ATA ACA GAT TCA TCT GAA GTG TAT GTT TCC CAA GTG ACG CAA AAA	1068
Gly Ile Thr Asp Ser Ser Glu Val Tyr Val Ser Gln Val Thr Gln Lys	
305 310 315	
GTT TTC TTT GAG ATA AAT GAA GAT GGT AGT GAA GCT GCA ACA TCA ACT	1116
Val Phe Phe Glu Ile Asn Glu Asp Gly Ser Glu Ala Ala Thr Ser Thr	
320 325 330	
GGC ATA CAC ATC CCT GTG ATC ATG AGT CTG GCT CAA AGC CAA TTT ATA	1164
Gly Ile His Ile Pro Val Ile Met Ser Leu Ala Gln Ser Gln Phe Ile	
335 340 345	
GCA AAT CAT CCA TTT CTG TTT ATT ATG AAG CAT AAT CCA ACA GAA TCA	1212
Ala Asn His Pro Phe Leu Phe Ile Met Lys His Asn Pro Thr Glu Ser	
350 355 360	
ATT CTG TTT ATG GGA AGA GTG ACA AAT CCT GAC ACC CAG GAG ATA AAA	1260
Ile Leu Phe Met Gly Arg Val Thr Asn Pro Asp Thr Gln Glu Ile Lys	
365 370 375 380	
GGA AGA GAT TTA GAT TCA CTG TGAATGAAAA GCACAGCCTC AGAATAAAAG	1311
Gly Arg Asp Leu Asp Ser Leu	
385	
ATGATTTCTC AAAAATAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1370

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Thr Ile Phe Leu Trp Ser Leu Leu Leu Phe Phe Gly Ser
-18 -15 -10 -5
Gln Ala Ser Arg Cys Ser Ala Gln Lys Asn Thr Glu Phe Ala Val Asp
1 5 10
Leu Tyr Gln Glu Val Ser Leu Ser His Lys Asp Asn Ile Ile Phe Ser
15 20 25 30

Pro	Leu	Gly	Ile	Thr 35	Leu	Val	Leu	Glu	Met 40	Val	Gln	Leu	Gly	Ala 45	Lys
Gly	Lys	Ala	Gln 50	Gln	Gln	Ile	Arg	Gln 55	Thr	Leu	Lys	Gln	Gln 60	Glu	Thr
Ser	Ala	Gly 65	Glu	Glu	Phe	Leu	Val 70	Leu	Lys	Ser	Phe	Cys 75	Ser	Ala	Ile
Ser	Glu 80	Lys	Lys	Gln	Glu	Phe 85	Thr	Phe	Asn	Leu	Ala 90	Asn	Ala	Leu	Tyr
Leu 95	Gln	Glu	Gly	Phe	Thr 100	Val	Lys	Glu	Gln	Tyr 105	Leu	His	Gly	Asn	Lys 110
Glu	Phe	Phe	Gln	Ser 115	Ala	Ile	Lys	Leu	Val 120	Asp	Phe	Gln	Asp	Ala	Lys
Ala	Cys	Ala	Glu 130	Met	Ile	Ser	Thr	Trp 135	Val	Glu	Arg	Lys	Thr 140	Asp	Gly
Lys	Ile	Lys 145	Asp	Met	Phe	Ser	Gly 150	Glu	Glu	Phe	Gly	Pro 155	Leu	Thr	Arg
Leu 160	Val	Leu	Val	Asn	Ala	Ile 165	Tyr	Phe	Lys	Gly	Asp 170	Trp	Lys	Gln	Lys
Phe 175	Arg	Lys	Glu	Asp	Thr 180	Gln	Leu	Ile	Asn	Phe 185	Thr	Lys	Lys	Asn	Gly 190
Ser	Thr	Val	Lys	Ile 195	Pro	Met	Met	Lys	Ala 200	Leu	Leu	Arg	Thr	Lys 205	Tyr
Gly	Tyr	Phe	Ser 210	Glu	Ser	Ser	Leu	Asn 215	Tyr	Gln	Val	Leu	Glu 220	Leu	Ser
Tyr	Lys	Gly 225	Asp	Glu	Phe	Ser	Leu 230	Ile	Ile	Ile	Leu	Pro 235	Ala	Glu	Gly
Met	Asp 240	Ile	Glu	Glu	Val	Glu 245	Lys	Leu	Ile	Thr	Ala 250	Gln	Gln	Ile	Leu
Lys 255	Trp	Leu	Ser	Glu	Met 260	Gln	Glu	Glu	Glu	Val 265	Glu	Ile	Ser	Leu	Pro 270
Arg	Phe	Lys	Val	Glu 275	Gln	Lys	Val	Asp	Phe 280	Lys	Asp	Val	Leu	Tyr 285	Ser
Leu	Asn	Ile	Thr 290	Glu	Ile	Phe	Ser	Gly 295	Gly	Cys	Asp	Leu	Ser 300	Gly	Ile
Thr	Asp	Ser 305	Ser	Glu	Val	Tyr	Val 310	Ser	Gln	Val	Thr	Gln 315	Lys	Val	Phe
Phe	Glu 320	Ile	Asn	Glu	Asp	Gly 325	Ser	Glu	Ala	Ala	Thr 330	Ser	Thr	Gly	Ile
His 335	Ile	Pro	Val	Ile	Met 340	Ser	Leu	Ala	Gln	Ser 345	Gln	Phe	Ile	Ala	Asn 350
His	Pro	Phe	Leu	Phe 355	Ile	Met	Lys	His	Asn 360	Pro	Thr	Glu	Ser	Ile 365	Leu

Phe Met Gly Arg Val Thr Asn Pro Asp Thr Gln Glu Ile Lys Gly Arg  
 370 375 380

Asp Leu Asp Ser Leu  
 385

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3974 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGTACCTAAG TGAGTAGGGC GTCCGATCGA CGGACGCCTT TTTTTTGAAT TCGTAATCAT	60
GGTCATAGCT GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG	120
CCGGAAGCAT AAAGTGTAAG GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG	180
CGTTGCGCTC ACTGCCCCGT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAATGAA	240
TCGGCCAACG CGCGGGGAGA GGCGGTTTGC GTATTGGGCG CTCTTCCGCT TCCTCGCTCA	300
CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG	360
TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAGGCC	420
AGCAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTTCCAT AGGCTCCGCC	480
CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC	540
TATAAAGATA CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC	600
TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA	660
GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTTC CTCCAAGCTG GGCTGTGTGC	720
ACGAACCCCC CGTTCAGCCC GACCGCTGCG CCTTATCCGG TAACTATCGT CTTGAGTCCA	780
ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG	840
CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA	900
GAAGAACAGT ATTTGGTATC TGCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG	960
GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC	1020
AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT	1080
CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCATGAGA TTATCGTCGA	1140
CAATTCGCGC GCGAAGGCGA AGCGGCATGC ATTTACGTTG ACACCATCGA ATGGTGCAAA	1200
ACCTTTCGCG GTATGGCATG ATAGCGCCCG GAAGAGAGTC AATTCAGGGT GGTGAATGTG	1260

AAACCAGTAA	CGTTATACGA	TGTCGCAGAG	TATGCCGGTG	TCTCTTATCA	GACCGTTTCC	1320
CGCGTGGTGA	ACCAGGCCAG	CCACGTTTCT	GCGAAAACGC	GGGAAAAAGT	GGAAGCGGCG	1380
ATGGCGGAGC	TGAATTACAT	TCCCAACCGC	GTGGCACAAC	AACTGGCGGG	CAAACAGTCG	1440
TTGCTGATTG	GCGTTGCCAC	CTCCAGTCTG	GCCCTGCACG	CGCCGTCGCA	AATTGTCGCG	1500
GCGATTAAAT	CTCGCGCCGA	TCAACTGGGT	GCCAGCGTGG	TGGTGTGCGAT	GGTAGAACGA	1560
AGCGGCGTCG	AAGCCTGTAA	AGCGGCGGTG	CACAATCTTC	TCGCGCAACG	CGTCAGTGGG	1620
CTGATCATTA	ACTATCCGCT	GGATGACCAG	GATGCCATTG	CTGTGGAAGC	TGCCTGCACT	1680
AATGTTCCGG	CGTTATTTCT	TGATGTCTCT	GACCAGACAC	CCATCAACAG	TATTATTTTC	1740
TCCCATGAAG	ACGGTACGCG	ACTGGGCGTG	GAGCATCTGG	TCGCATTGGG	TCACCAGCAA	1800
ATCGCGCTGT	TAGCGGGCCC	ATTAAGTTCT	GTCTCGGCGC	GTCTGCGTCT	GGCTGGCTGG	1860
CATAAATATC	TCACTCGCAA	TCAAATTCAG	CCGATAGCGG	AACGGGAAGG	CGACTGGAGT	1920
GCCATGTCCG	GTTTTCAACA	AACCATGCAA	ATGCTGAATG	AGGGCATCGT	TCCCCTGCG	1980
ATGCTGGTTG	CCAACGATCA	GATGGCGCTG	GGCGCAATGC	GCGCCATTAC	CGAGTCCGGG	2040
CTGCGCGTTG	GTGCGGATAT	CTCGGTAGTG	GGATACGACG	ATACCGAAGA	CAGCTCATGT	2100
TATATCCCGC	CGTTAACCAC	CATCAAACAG	GATTTTCGCC	TGCTGGGGCA	AACCAGCGTG	2160
GACCGCTTGC	TGCAACTCTC	TCAGGGCCAG	GCGGTGAAGG	GCAATCAGCT	GTTGCCCGTC	2220
TCACTGGTGA	AAAGAAAAAC	CACCCTGGCG	CCCAATACGC	AAACCGCCTC	TCCCCGCGCG	2280
TTGGCCGATT	CATTAATGCA	GCTGGCACGA	CAGGTTTCCC	GACTGGAAAG	CGGGCAGTGA	2340
GCGCAACGCA	ATTAATGTAA	GTTAGCGCGA	ATTGTCGACC	AAAGCGGCCA	TCGTGCCTCC	2400
CCACTCCTGC	AGTTCGGGGG	CATGGATGCG	CGGATAGCCG	CTGCTGGTTT	CCTGGATGCC	2460
GACGGATTTG	CACTGCCGGT	AGAACTCCGC	GAGGTCGTCC	AGCCTCAGGC	AGCAGCTGAA	2520
CCAACCTCGC	AGGGGATCGA	GCCCCGGGTG	GGCGAAGAAC	TCCAGCATGA	GATCCCCGCG	2580
CTGGAGGATC	ATCCAGCCGG	CGTCCCGGAA	AACGATTCCG	AAGCCCAACC	TTTCATAGAA	2640
GGCGGCGGTG	GAATCGAAAT	CTCGTGATGG	CAGGTTGGGC	GTCGCTTGGT	CGGTCATTTT	2700
GAACCCAGAG	GTCCCGCTCA	GAAGAACTCG	TCAAGAAGGC	GATAGAAGGC	GATGCGCTGC	2760
GAATCGGGAG	CGGCGATACC	GTAAAGCACG	AGGAAGCGGT	CAGCCCATT	GCCGCCAAGC	2820
TCTTCAGCAA	TATCACGGGT	AGCCAACGCT	ATGTCCTGAT	AGCGGTCCGC	CACACCCAGC	2880
CGGCCACAGT	CGATGAATCC	AGAAAAGCGG	CCATTTTCCA	CCATGATATT	CGGCAAGCAG	2940
GCATCGCCAT	GGGTCACGAC	GAGATCCTCG	CCGTCGGGCA	TGCGCGCCTT	GAGCCTGGCG	3000
AACAGTTCGG	CTGGCGCGAG	CCCCTGATGC	TCTTCGTCCA	GATCATCCTG	ATCGACAAGA	3060
CCGGCTTCCA	TCCGAGTACG	TGCTCGCTCG	ATGCGATGTT	TCGCTTGGTG	GTCGAATGGG	3120

CAGGTAGCCG GATCAAGCGT ATGCAGCCGC CGCATTGCAT CAGCCATGAT GGATACTTTC	3180
TCGGCAGGAG CAAGGTGAGA TGACAGGAGA TCCTGCCCCG GCACTTCGCC CAATAGCAGC	3240
CAGTCCCTTC CCGCTTCAGT GACAACGTCG AGCACAGCTG CGCAAGGAAC GCCCGTCGTG	3300
GCCAGCCACG ATAGCCGCGC TGCCTCGTCC TGCAGTTCAT TCAGGGCACC GGACAGGTCG	3360
GTCTTGACAA AAAGAACCGG GCGCCCCTGC GCTGACAGCC GGAACACGGC GGCATCAGAG	3420
CAGCCGATTG TCTGTTGTGC CCAGTCATAG CCGAATAGCC TCTCCACCCA AGCGGCCGGA	3480
GAACCTGCGT GCAATCCATC TTGTTCAATC ATGCGAAACG ATCCTCATCC TGTCTCTTGA	3540
TCAGATCTTG ATCCCCTGCG CCATCAGATC CTTGGCGGCA AGAAAGCCAT CCAGTTTACT	3600
TTGCAGGGCT TCCCAACCTT ACCAGAGGGC GCCCCAGCTG GCAATTCCGG TTCGCTTGCT	3660
GTCCATAAAA CCGCCCAGTC TAGCTATCGC CATGTAAGCC CACTGCAAGC TACCTGCTTT	3720
CTCTTTGCGC TTGCGTTTTT CCTTGTCAG ATAGCCCAGT AGCTGACATT CATCCGGGGT	3780
CAGCACCGTT TCTGCGGACT GGCTTTCTAC GTGTTCCGCT TCCTTTAGCA GCCCTTGCGC	3840
CCTGAGTGCT TCGGCAGCG TGAAGCTTAA AAACTGCAA AAAATAGTTT GACTTGTGAG	3900
CGGATAACAA TTAAGATGTA CCAATTGTG AGCGGATAAC AATTTACAC ATTAAAGAGG	3960
AGAAATTACA TATG	3974

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAGCTTAAAA AACTGCAAAA AATAGTTTGA CTTGTGAGCG GATAACAATT AAGATGTACC	60
CAATTGTGAG CGGATAACAA TTTCACACAT TAAAGAGGAG AAATTACATA TG	112